

Chickens First

Speciation by “Hopeful Monsters” in Fraternal Supertwins

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Abstract

The idea of “hopeful monster” was proposed by Goldschmidt who envisioned that speciation could occur instantaneously via major chromosomal rearrangement in a one-step process; but he could not unravel how similar individual in the opposite sex to appear on the same time and location to generate next generation. This paper provides the answer for the challenge.

In this paper, a model of speciation in animals is discussed in detail. Only four steps are needed to generate a new species in sexual animals: fraternal twin zygotes, similar gross mutation on the zygotes, self-splitting of mutated zygotes into two groups of identical zygotes of both sexes, development of zygotes with birth of babies, and inbreeding when they mature. The outcome of these steps is generation of new species with chromosomal homozygosity. Viviparous animals (living young not eggs are produced) are used to explain the model. With slight modifications, other asexual organisms could be accommodated.

As the model provides the simplest explanation for speciation in all sexual animals, which plausibly explains many puzzles in biology; such as chicken egg, Cambrian explosion, appearance of new organs, etc. The author presents a few predictions that can be falsified.

This model needs only one assumption and it is consistent with many well-known observations.

Introduction

Speciation, or the generation of a new species, is an essential but unsolved issue in evolutionary biology. Although many prominent evolutionists have claimed to unravel the puzzle, the mechanism of speciation remains a hot debate (Coyne and Orr 2004; Howard and Berlocher 1998; Margulis 2003a; White 1978). As recently as 1974 Lewontin said, “We know virtually nothing about the genetic changes that occur in species formation.” This statement is, unfortunately, largely still true today.

Two schools of thought on evolutionary mechanisms exist. The first is gradual one, such as Darwinian natural or sexual selection and geographical isolation, the second is instantaneous one such as polyploids and virgin birth. The “classical” models of speciation are reproductive isolation from selection or geographical isolation, and hold that the instantaneous speciation has played little or no role in mammal evolution (Mayr 1988).

Goldschmidt recognized that significant morphological reorganization could occur with major chromosomal rearrangement, which generates the “hopeful monster”: the random emergence of an individual carrying major genetic and morphological novelty as a new species, but had problems to tell how similar individual in the opposite sex to appear on the same time and location (Goldschmidt 1940).

The idea of this paper is simple. In order for a mutation to be hereditary, it has to be present in fertilized eggs. How the mutation will affect the zygotes is dependent on internal and microenvironmental factors, which could generate a new species without natural selection or geographical barriers. Natural selection affects a new species only after its birth. The members of new generated species have to mate with individuals of their species in the same time and location to reproduce next generation. To accomplish this task, the author proposes a simple mechanism with only four steps: fraternal twin zygotes, similar gross mutations on the zygotes, self-splitting of mutated zygotes into two groups of identical zygotes in both genders, development of zygotes with live births and inbreeding when they mature.

The model provides sound explanations to many biological mysteries, and it presents several testable predictions.

Model of speciation: gross mutant in cluster and mutants inbreeding (GMCMI)

The proposed mechanism of speciation has four major steps.

1. Formation of two fertilized eggs of the opposite sex

Animal development begins when a sperm fertilizes an egg to form a zygote. Fraternal twin’s zygotes are formed when two eggs are each fertilized by a single sperm. Fraternal twins are common natural phenomena across almost all bisexual animals.

2. Gross mutations on the zygotes

In fertilized eggs, DNA synthesis is active and these eggs are extremely sensitive to mutagens. The nature of mutations is determined by the nature of mutants and the

microenvironments around the zygotes. The mutation could be minor, thereby causing little harm, or a gross one, which will cause failure of mating with ancestral species. A gross mutation is defined by its outcome: any modifications on the DNA structure will be the gross mutation, if it leads to failure of bivalent binding between the ancestral and descended haploid chromosomes. The gross mutation does not necessarily lead to gross physical changes of the involved organism or speciation. Many, if not all, chromosomal rearrangements, such as deletions, duplications, translocation, and karyotypic fission have the potential to be gross mutations, and only gross mutation can lead to speciation. These mutations could occur at one locus or multiple loci.

3. Self-replication of fertilized eggs

The mutant zygotes can self-replicate to form mixed multiple identical zygotes with gross mutations, which could develop into mixed identical supertwins with a gross mutation.

4. Mating among the siblings from the same gestation

The majority of the mutants would die during the embryonic stage, leaving a very small number to survive. Of these, even a smaller number would mature to adulthood. The characteristics of the novelties are determined by how the mutations occur. The mutations would be not only demonstrated in the somatic cells of offspring with the novel characteristics, but also inherited, and passed onto their gamete cells.

The newcomers live together, and have the similar anatomical structures. Neither pre-zygotic nor post-zygotic reproductive barriers are present among the fraternal siblings. Inbreeding would be natural among these siblings with the reproductive second generation as the outcome. In the whole process, only step two is an assumption, while the remaining three steps are natural daily phenomena. I named the model gross mutant in cluster and mutants inbreeding (GMCMI).

Evidences to support the model

Several pieces of evidence support validity of the model and below a few are discussed.

A. Polyploids

A polyploidy organism has more than two copies of each of its chromosomes. More than half of all land plants species are polyploids, including wheat, corn, and cotton. It is estimated that up to 85-95% ferns and many other plant species were generated by polyploids (Grant 1994; White 1978). Speciation via polyploidy is instantaneous, and only takes just one generation. Moreover, the new species are not spatially separated from its ancestors.

Speciation through polyploidy occurs less often in animals, but it still exists (Gallardo 1999). Speciation through animals may occur in a number of insect species including walking sticks, grasshoppers, blackflies, and beetles (Gregory 2005).

Even there are several model to explain the mechanism of polyploids, nobody has proposed the twin mutation model, which would explain all speciation in bisexual plants and animals, including polyploids. Instantaneous speciation in both plants and animals

are excellent sources to validate the GMCMI model, which holds that all species arise promptly in the same location as their ancestors.

B. Virgin birth

Parthenogenesis, which has been seen in about 70 species, including snakes and lizards, is a process in which eggs become embryos without male fertilization. Many annoying insects such as ants, bees, wasps, aphids as well as some fleas and ticks create progeny in this manner. Many of these species are believed to be descended from sexually reproducing ancestors (Schlupp 2005; Simon and Rispe, Claude & Sunnucks, Paul 2002).

A female white spotted bamboo shark at the Belle Isle Aquarium in Detroit surprised zookeepers in July by giving birth to two babies. It was a virgin birth or parthenogenesis as she had not been near a male shark for six years (Mayell 2002).

The resulting animals are different species from their direct sexual ancestors, they are asexual animals, and the same principle is applicable, i.e. instantaneous speciation.

C. Correlation between number of species and litter size

It is estimated that 20 to 30 million species of insects inhabit the earth, but only over 1 million of them are named and described. Some insects have their offspring from a single egg, termed polyembryony, in which two or more young result from a single egg. This mechanism is similar to how monozygotic twins originate in humans. Some parasitic wasps have eggs that keep on dividing, resulting in as many as 1,500 to 2,500 young from a single egg (Chauvin 1967; Grimaldi and Engel 2005).

Only about 4,000 of the animal species are mammals but there are almost 3,500 species of cockroaches. Majority of mammals has litter sizes ranging from one to a few dozens and many large mammals have single birth. This limitation makes it very unlikely for them to branch into new species.

In the model, the new animals are generated by mixed polyembryony, larger litter size, and speciation occurs more easily. The model accurately predicts that there will be more insect species than mammal species.

D. New species are found within decades

By the classical evolution theory, speciation should be a very slow process. As Mayr stated:

“Speciation, except for polyploidy and some other chromosomal process, is too slow to be observed directly. Owing to the slowness of the speciation process, it is not possible to study the same individual or population “just before” and just “after” speciation (Mayr 1988).

However, new species were constantly discovered and they did not require thousands of generations, but only a few decades. For instance, Fishelson in Eilat in 1975 looked at the morphology of 80 *Pterois volitans*. None of the specimens had a spotted, feather-like tentacle, although five specimens did have wider tentacles than normal. A follow-up study on the same reefs in Eilat found two new forms of lionfish among the 35 specimens examined. These fish had the eyespot on just a single tentacle. Subsequently, the feather-like tentacle form has been found outside the Red Sea in the Pacific Ocean (Fishelson 2006). The rates of speciation in cichlids has been astonishingly fast since the

discovery of five endemics in Lake Nabugabo, a small lake that is less than 4000 years old and separated from Lake Victoria. These five species are believed to have close relatives in Lake Victoria and they chiefly differ in the male's breeding coloration (Greenwood 1965). Even faster rates of speciation were suggested by the finding that the southern end of Lake Malawi was arid only two centuries ago and it is now inhabited by numerous endemic species and 'color morphs'. These are believed to have originated during the last 200 years! (Meyer 1993). One observation relates to the description of a new Mexican cichlid, a new species, which is named *Paratheraps breidohri* by the authors, would be formed in less than 30 years old (Werner, U. & Stawlkowski, R. 1988). Salmon in a United States lake split into two separate populations in just 13 generations, or about 60-70 years (Hendry, Andrew P. and Wenburg, John K 2000).

Madeira is a rugged volcanic island with sharp black cliffs that block all but a few isolated rocky shores. The Portuguese first inhabited the island in the 15th century and they inadvertently dropped small groups of mice at each stop. Janice Britton-Davidian, a France evolutionary biologist, caught hundreds of small brown mice that appeared alike but were genetically distinct. The common brown house mouse of Europe, presumably the ancestor of the Madeira mice has 40 chromosomes. Britton-Davidian found six distinct populations that had from 22 to 30 chromosomes (Britton-Davidian and others 2000).

It is very difficult to visualize how this kind of speciation occurs by changes of allele frequencies or geographical isolation within such a short time. However, they are all consistent with the model that all speciation occurs by one generation. It, however, may require a few or many generations for them to be discovered.

E. Numerous biologists support mechanism of instantaneous speciation

Many well-known biologists and geneticists support the idea of instantaneous speciation. In 1889, Hugo de Vries, a Dutch botanist had hypothesized the existence of "pangenes" (now called "genes") and argued for a saltationist mechanism of evolution, with selection only operating to produce local varieties. Bateson recognized minor differences among each individual, but the change for new species is discontinuous in the sense that new features arise rapidly. For Morgan, a new feature could arise because of a single mutation, and a novel characteristic could arise by way of a single mutation, and, therefore, a new species could also does (Schwartz 1999).

"Species and the higher categories originate in single macroevolutionary steps as completely new genetic systems (Goldschmidt 1940)".

"Is it realistic to think that an entire population may stem, via sexual reproduction, from a single fertilized female individual? The necessity of sib mating the progeny of the founder individual poses no impenetrable genetic or other biological barrier to survival and reproduction. The extreme, naturally occurring case, wherein a population is founded by a single such propagule, is not only biological feasible but also provides a degree of operational simplicity for theoretical purposes (Carson 1984)".

"Mutation accumulation does not lead to new species or even to new organs or new tissues. Rather the important transmitted variation that leads to evolutionary novelty comes from the acquisition of genomes. Entire sets of genes, indeed whole organisms each with its own genome, are acquired and incorporated by others (Margulis 2003b)."

The idea of gross mutation and instantaneous speciation are consistent with the insights of previous research. The biggest challenge is how to adequately address the problem of ensuring that more than one “hopeful monster,” of each sex, at the same time and place. This is a necessity because, for sexually reproducing organisms, at least one male and one female of a new species are required for the species to become established. The model is just filling a gap in knowledge.

Role of Natural selection

Three types of natural selection are known. Every organism has its own natural environment to live in which proper food, temperature, and air is provided. If the species that required a high temperature was born in a cold climate, then it would not survive, and would be selected out by natural condition. This is known as type I natural selection. This type of natural selection also includes natural events, such as fire, flooding, or earthquake. Any individual could be the target of these accidents. Outcome from this selection would not change allele frequency of population.

In type II natural selection, individuals possessing favorable characteristics will tend to compete more successfully with their unlikely peers. They will have more mating partners and leave more descendants than their less fortunate counterparts. Even if the allele frequency is modified, the less fortunate and their progeny may still survive. The Neo-Darwinists usually consider this natural selection. However, this type of natural selection only modifies allele frequencies within a species, and it does not eliminate species or generate a new species.

As the space and resources of the environment are not unlimited, occasionally sufficient food might be not available to the whole population. In Darwin’s model, competition for limited resource within and between populations will generate new species because of the survival of the fittest. This is type III natural selection. Type III selection nature can occur theoretically, which is not ubiquitous. In the proposed model, Type III natural selection could occur theistically, but it can cause death of certain members within species and never leads to speciation.

In initial phase, all members of new species are homogenous, and only type I natural selection functions. When heterogeneity has developed within a species, type II natural selection will occur. Food might never become scarce, even competition might exist, and type III natural selection might never function.

In human society, war is usually initiated by conflict of faith, desire to control power and land, and misunderstanding, rather than lack of food. Starvation is usually caused by political reasons, not for lack of natural resource itself.

“No evidence in the vast literature of heredity change shows unambiguous evidence that random mutation itself, even with geographical isolation of populations, leads to speciation (Margulis 2003a).”

Puzzles and Answers

The model provides sound explanation to many mysteries in biology, which is not available to other evolutionary theories.

A. Chickens first

The chicken or egg paradox has persisted for many centuries. Current popular evolutionary theories do not provide any plausible explanation for it and often do not

mention it at all. By the model, the initial members of chickens or “hopeful monsters” evolved from a pre-chicken ancestor through gross mutations at the zygote stage. The modified zygotes were the beginning of the first chicken at the one-cell stage. The cells (two zygotes) self-replicated, proliferated, and eventually became male and female chickens. Their somatic cells had the characteristics of chickens, while the gonads in adult chickens would produce chicken gametes. Therefore, chickens or “hopeful monster”, or a group of chickens or “hopeful monster”, must have come first, which are derived from zygotes, not from eggs.

B. Lack of transitional links

Numerous problems arise from assuming natural selection the mechanism for speciation. The most troubling aspect was the lack of a transitional species in the fossil records (Gould, Stephen J. and Eldredge, Niles 1977). By the GMCM model there should be no or few intermediate fossils. Multifactorial explanations can be applied. The novelties generated by the gross mutation could produce huge genotypic and phenotypic changes. Second, if speciation were the result of the gross mutations at the individual level, the speed of evolution would be faster than one under natural selection and the quantity of intermediates would be too small to be detected in fossils. Third, speciation occurs at very narrow geographical locations and is compatible with the absence of intermediate fossils. Fourth, the newcomers must recognize each other for mating. Non-continuous or distinct characters might be necessary for recognition. The model predicts distinct features exist between species in evolution process, not otherwise.

C. Cambrian explosion

The fossil records show that primitive life on Earth began about 4 billion years ago. At the beginning of the Cambrian period 545 million years ago, all the major anatomical structures seem today evolved in a span of only 5 to 10 million years in an event known as the Cambrian explosion (Gould 1989).

The model does not offer any clues of the “seeds” regarding how they were generated, as this is not relevant to any theory of speciation. The model is the mechanism of speciation with assumption that ‘seeds’ or spores of organism pre-existed. The pattern of the growth predicted by the model is consistent with what we observed in the Cambrian explosion. Under proper conditions, the original seeds became primitive organisms, which multiplied, become a viable species, and reproduced the next new species. The circle would continue in an explosive pattern as shown in the initial phase of the Cambrian explosion. Nevertheless, the trend could not last forever as ecological niches decreased and food supplies were depleted. All of these might be contributed to the decreased exploration as phyla were lost and not replaced.

D. Organs and environments

Fish living in underwater caves are blind and have apparent scars where their eyes should be. The eyes of the Mexican tetra have a lens, sclera with a degenerate retina, and optic nerve. Although the tetra cannot see, but have eyes with retinas and lenses, and the eyelids grow over the eyes to seal them from outside light. Other than the lack of sight, these cave dwelling fishes are identical to fish living at the water’s surface that are sighted (Durand and others 1993; Jeffery 2001).

It is thought that a group of fish with normal eyes was trapped while swimming in an underground cave. Without light stimulation, their eyes atrophied and, over the generations, they become blind. However, even in the darkness, the genetic codes in trapped fish would have retained its programming to develop eyes. The genes would be unaware that eyes were no longer required.

The model provides a more plausible explanation. Gross mutations occurred in the ancestral fish with production of eyeless fish. Some fish went to the surface and did not survive, because they could neither find food nor escape predators. Some of them swam into lightless caves where not having eyes was not a disadvantage. Fish with normal eyes were at a disadvantage as their eyes would be subject to injury from hitting the rocks and cave walls in the darkness. Only eyeless fish that remained in the caves flourished.

E. Drug resistant bacteria

A drug resistant bacterium has been widely cited as the evidence to support of Darwin's idea of evolution. Ernst May wrote:

“When penicillin was first introduced in the 1940s, it was amazingly effective against many types of bacteria. Any infection, let us say by streptococci or spirochetes, was almost immediately cured. However, bacteria are genetically variable and the most susceptible ones succumbed most rapidly. A few that had acquired by mutation genes that had made them more resistant survived longer and a few still had survived when the treatment stopped. In this manner, the frequency of somewhat resistant strains gradually increased in human populations. ...Thus by gradual evolution an almost completely susceptible species of bacteria had evolved into a totally resistant one (Mayr 1991)”.

Several issues are present here. First, bacteria cannot be categorized as a new species, because they reproduce asexually. Bacteria with different characteristics are often considered a 'strain' in microbiology, rather than a distinct species. Many subgroups or strains are generated by random genetic mutations, and are found within any type of bacteria. One strain happens to be penicillin-resistant and confers the strain a growth advantage over penicillin-sensitive bacteria under the drug. Second, even if drug-resistant bacteria are distinct species, its arrival might not be associated with natural selection or antibiotics at all. The drug-resistant organism might have existed long time before the advent of antibiotics through random mutations or plasmid transduction (Ochman and Lawrence, Jeffrey M. & Grolsman, Eduardo A. 2000). The application of antibiotics would kill other bacteria while the drug-resistant strain easily proliferated and they are singled out.

F. Atavisms

Anatomical atavism is a structure that was once found in a remote ancestor but now lost in a recent lineage. For example, if horse occasionally displayed gills, then this would be a potential atavism, because gills are pathognomonic of taxa (e.g. fish), to which horses do not belong. For developmental reasons, the occasional occurrence of atavisms is expected under common descent, if the structures or functions were lost between ancestor and descendant lineages (Hall 1995).

Atavisms also occur at molecular levels. Humans do not have the capability to synthesize vitamin C, which, if deficient in the diet, will lead to scurvy. The predicted ancestors of humans could synthesize vitamin C as do most other animals, except

primates and guinea pigs. The L-gulano-g-lactone oxidase gene, the gene required for vitamin C synthesis was found in humans and guinea pigs as a pseudogene and other primates (Ohta and Nishikimi 1999). Classic evolutionary theories rarely provide any plausible explanation for how atavisms occur should they be selected out under natural selection.

By the model, gross mutations might affect both structural and regulatory genes responsible for certain organs or chemical products. If only regulatory genes that controlled growth were affected, the organs would not develop in the new animals and the structural genes of these organs might be still intact. The regulatory genes could be reactivated in the descendant lineages; thus, the lost organs would reappear. It is conceivable that the structural genes for other vitamins still exist in humans as pseudogenes.

Prediction and falsification

The strength of any scientific theory is its ability to generate testable predictions. These predictions are then compared with established data to determine how consistent theory is with these data. Testability lies at the heart of the scientific enterprise, which is based on unique, specific prediction. In principle, a scientific hypothesis should rule out conceivable possibilities, which is the essence of the Popperian falsifiability criterion (Popper 2002). The model can provide many valid predictions.

1. Every species has two “Eves”

Prediction

According to the model, every species have two Eves. The first one is a single ancestral mother, who gives birth to the initial members of a new species. On the other hand, the second “Eve” or ‘Eves” is a group of females with very similarly genetical structure, who are the first generation or “seed” of new species. Since the first “Eve” was the single individual in the history, no scientific methods can identify it. Every species are from the second “Eve”. Laboratory studies of mtDNA could show all sexual species are traced to a single mother or group of female with similar genomic structures.

Evidence

In 1987, University of California geneticist Allan Wilson announced the results of a study utilizing mitochondrial DNA as a marker to trace the ancestry of modern humans. They collected and analyzed mtDNA material from 147 women from Africa, Asia, Europe, Australia, and New Guinea. Their findings support the conclusion that “the common ancestor of modern humans lived in Africa, about 200,000 years ago (Cann, Stoneking, Wilson 1987)”.

The only way to test the story of mitochondrial Eve was to trace the ancestry by using the Y chromosome to determine if separate lines of evidence also led back to African ancestors, as the human Y chromosome is strictly paternally inherited and, in most of its length, does not recombine during male meiosis. Michael Hammer at the University of Arizona surveyed noncoding region of the Y chromosome in 1544 men worldwide and found the same pattern in Haplotype 1A (Gibbons 1997).

Falsification

Similar studies can be performed in other sexual species. If we could confirm multiple origins of geographical locations for any sexual species, it would be catastrophically problematic for the GMCMI model.

2. Similar mtDNA sequences among initial members of species

Prediction

As speciation occurs with only a few members randomly, it is almost impossible to identify what the new species is, where and when it formed. There are many newly found species reported each year, some of them are old species, just discovered recently, some of them are newly formed species.

By this model, all species had similar mitochondria in females and Y chromosomes in males at the beginning. Statistically, the mitochondrial DNA should be more homologous in the newly found species, comparing with other well known old species.

Evidence

Lake Victoria is youngest of the three large lakes in East African, formed about 250, 000 to 750.000 years ago. It contained over 300 endemic cichlids. The mtDNA variation among fish of the Victoria flock was found to be very small as no variation was detected in 363 base pairs of the cytochrome b gene (Johnson and others 1996).

Falsification

If lab results show less diverse mtDNA in multiple well-established species than what is present in the newly found species, then the model would have failed.

3. Inconsistency of molecular phylogeny

Prediction

Based upon Darwin's theory, phylogenetic trees should be approximately the same regardless of which molecules are chosen for comparison, whereas by the models, speciation is the outcome of gross mutations by a random process. No specific patterns explain how, why, where the mutations occur, and only few segments of DNA structures could be involved in each event of speciation, leave the rest of genome much less modified.

Study genomic structure within same species will show gross irregularities of genes and inconsistency in molecular phylogeny is a rule, not an exception.

Evidence

A variety of genes from different organisms demonstrated that their relationships contradicted the evolutionary tree of life derived from rRNA analysis. Different molecules lead to different phylogenetic trees. According to biologist Carl Woese, an early pioneer in constructing rRNA-based phylogenetic trees, "No consistent organismal phylogeny has emerged from the many individual protein phylogenies so far produced. Phylogenetic incongruities can be seen everywhere in the universal tree, from its root to the major branching within and among the various [groups] to the makeup of the primary groupings themselves (Dolittle 2000)."

Falsification

Many whole genome sequences have become available. By comparing different genes across several species, ones could compare molecular data of phylogenetic trees.

These data should show inconsistency in some genes or proteins much more prominent than others should. Consistency among many genes will challenge the model.

Discussion

The frequent occurrence of karyotypic differences among related species in many groups of organisms suggests that the karyotypic changes or chromosomal alterations lead to speciation.

Neo-Darwinian evolutionists cannot accept that all speciation are saltational process.

“The claim, for instance, that all speciation is due to chromosomal reorganization was refuted by Carson (1975), who showed that active speciation in Hawaiian Drosophila can take place without any visible change in the chromosomes. Since these Hawaiian species can be analyzed in great detail with the help of their giant salivary chromosomes, whatever structural chromosomal changes may occur during speciation must be very minute(Mayr 1982)”.

The answer to the critics is that karyotypic changes detected under microscope usually mean 1 to 2 million base pairs (Passarge 2001), the gross mutations at chromosomal level might span from few thousands to hundreds millions base pairs, and many gross mutations are submicroscopic. Some types of chromosome change may only cause chromosomal polymorphisms without speciation while the other chromosomal changes would lead to speciation.

The models explain negative heterotic, unbalanced gametes, and structural chromosomal heterozygosity due to underdominant chromosomal changes that represent a barrier for acceptance of chromosomal speciation.

According to Darwin, speciation is outcome of variation AND natural selection. In modern Neo-Darwinian words, variation means genetic variation, speciation is still a two-step process in which mutations occur randomly and instantaneously, and natural selection is a must for speciation that lasts very, very long, in matter of million years.

The author proposes that all biodiversity (speciation) occur instantaneously via the gross mutation and speciation is just a one-step process. Mutation is both necessary and sufficient for speciation. As the newcomers arrive in small numbers and both genders, it might take many generations for them to be populated and discovered.

Assume that a chimpanzee is a direct ancestor, which has 48, or 24 pairs of, chromosomes. Zygotes in a chimpanzee female might mutate and its chromosomes reduce to 46, or 23 pairs, then the organism with 46 chromosomes was born as a human and no natural selection was involved before the birth.

About 10% of human couples in reproductive age experience infertility, which has several known etiologies. One of them is chromosomal abnormality, which accounts for 10-25% infertility in human; there might be much more at submicroscopic levels (Katz 2007). About 0.6% of unselected newborns have a demonstrable chromosomal abnormality. Individuals with a chromosomal alteration may appear normal and even have a normal life span. However, by the biological concept of species, these individuals are not the same species as other members of humans, as they cannot breed with them and have fertile offspring.

Basic genetics demonstrate mutation basis for any novelties, whether novelties is eye color, height or total new species. Member with one color eye can mate with other

members with different colors eye within same species. The frequency of eye color is determined by allele frequency, which would be affected by natural selection. However, new species have to mate with members of the same species to proliferate before natural selection can occur. No other evolutionary theories provide a sound explanation for how the partners within the same species are generated.

Like many other scientific concepts, such as electron, quark, or entropy, the model implies that speciation is not observable, which can only be inferred by reasoning. Speciation cannot be studied by allele frequency, incipient species does not exist.

Many evolutionists accept “geographical isolation” put forward by Mayr as the major influential factor in speciation. The general position adopted by Mayr is that almost all speciation is allopatric, i.e., that geographical isolation of the population is a necessary for speciation. Mayr viewed that allopatric speciation might be the most common mechanism; however, this idea is not falsifiable, even all new species found so far are instantaneous and sympatric. The denominator or, how many species has been formed in the past, is unknown. Moreover, data to support allopatry can also be interpreted by sympatry (Coyne and Orr 2004).

Speciation by founder effect and drifting (Grantham 1995; Templeton 1980) would face the same unanswered challenge as “hopeful monster”: how the novelties get mate and reproduce? Newcomers would not accumulate if not-reproductive with proper partners.

In biology, almost everything plays by chance, not by certainty. By the model, speciation is only an event (gross mutation); the number of such event might be astronomical, as new species could be generated from every single mother with fraternal twins in every childbirth. In a hypothetical case: there was an animals with large litter size that survived for one million years in the world, during which there were one millions births yearly on average, the number of the total births was 1 trillion. Assuming the rate of gross mutation was 0.1% in zygotes, one of a million was the similar mutation in these twin zygotes, 1% the mutated zygote survived and populated successfully. The number of new species would be ten ($10^{12} \times 10^{-3} \times 10^{-6} \times 10^{-2}$). Even the odds in each step are very, very small, but it is still possible that one species generates multiple species after factoring in all these odds. Only the survivors are observed, and they are in the numerator; a billion times more in the denominator that failed in these processes, which were never known. Species might be one of the luckiest among million failures.

Scant evidence supports the bottleneck speciation in laboratory experiments. Five small-scale and three large-scale studies have failed to generate positive results (Rice and Hostert 1993). Gross mutations in zygotes under natural conditions might differ from the ones obtained under experimental conditions. Millions of failure might occur prior to a successful one that would make successful laboratory speciation very unlikely.

Initial number in new species not necessarily means only a few members; it could be hundreds or thousands depending on the species. Polyembryony can generate thousands identical supertwins in insects (Craig, Slobodkin, Wray, Gregory A. and Biermann, Christiane H. 1997; Grbic 2003).

Ring species consist of two reproductive isolated forms connected by chain of intergrading populations. Salamanders (*Ensatina eschschotlzil*) and the greenish warblers (*Phylloscopus trochiloides*) are the two most studies ring species (Irwin, Irwin, & Price, Trevor D. 2001; Irwin, Bensch, Irwin, Jessica H., Price, Trevor D. 2005; Stebbins 1949).

The conclusion that they are different species is based on the lack of observable mating among them. However, mating is complicated behavior, which is affected by many factors, such as communication, morphology, and movement patterns. Differential mating occurs even within the same species. The more they differ in their affecting factors, the more unlikely successful mating is. It is almost certain that there is a mating problem among those who speak only Mongolian and those who only speak Portuguese, if one only mixes them together; however, there are no evidences to support those groups of persons heading to different species.

As the time length implicated in the gradual process would be several hundred thousand years, if it would occur and it is impossible for the whole process to be observed and confirmed. Faced with so many cases of instantaneous speciation, the consensus among many evolutionary biologists is to favor plural mechanisms in speciation.

Evolution is an opportunistic process.... Pluralism is characteristic of all aspects of the evolutionary process. Reproductive isolation is effected in most higher animals by prezygotic isolating mechanisms (e.g., behavior), and in others by chromosomal incompatibilities, sterility, or other postzygotic factors. Speciation usually occurs for geographic reasons in terrestrial vertebrates, but it is sympatric in certain groups of fishes and perhaps in plant-host-specific groups of insects (Mayr 2001).

The problem with this position is that no scientific methods can disprove these gradual models. Even all cases are instantaneous ones, possibility always exists that next one, or one in the past is by gradual process. Scientists usually use “Occam’s Razor” in pursuit of truth (Milner 1990). It states, “Entities are not to be multiplied without necessity.” The model can be applied to all sexual organisms; assuming the existence of other unproven models is unnecessary, plus these models do not provide sound explanations for many biological issues discussed above.

Summary

The proposed model has five elements: the twin zygotes, the gross mutation, self-replication, supertwins, and inbreeding. These observable phenomena occur at any time and place. The challenge is not whether speciation happens by the proposed model, but how to detect these new species at the initial stage.

Based upon Darwin's theory, speciation is a two-step process consisting of variation and natural selection, and it is a gradual population phenomenon (Mayr 1991). In the models discussed, speciation is only a one-step process; thus, only mutation itself is required for speciation. Natural selection only works on variants of pre-existing species, and it has no creating power, and only eliminates the unfit. Phyletic speciation through natural selection or geographical isolation never occurs.

The model has provided sound explanation to numerous mysteries in biology with only one premise in the model. Given the chicken and egg paradox, mosaic of evolution, missing fossils linking, and many others, it would be inconceivable for other evolutionary theories to answer these puzzles with such a simple and plausible idea.

Prediction is essential element for true scientific idea. Several predictions are testable by the model. The predictions have numerous laboratory evidences, and the proposed falsifications are from several perspectives as well as specific and unique without alternative explanations.

Mutation is a random, rare, unpredictable event; it is extremely unlikely for any similar mutation to occur at same time and place if they are in completely unassociated situations. Occurrence of at least two similar novelties is essential for survival of any new species. The model makes occurrence similar mutations occur much more likely than one otherwise, as the zygotes are at very close or even glued together. Factors affecting the nature of mutation should be very similar or identical. The twin zygotes model is to convert two independent random processes into two linking, and non-independence ones. More than that, the newcomers were born at same time, raised at same location; there should be little or no temporal and geographical reproductive barriers among them.

It is emphasized that ones should not criticize Darwin; genetic studies did not exist 140 years ago, embryology was in its primitive stage and species concept was based on morphology, not on biology. All of these factors prevented illustration of the correct mechanism of evolution.

"Nothing in biology makes sense except in the light of evolution (Dobzhansky 1997)".

However, this statement only becomes convincing after the correct mechanism is known.

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